



SEQUENCE LISTING

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<120> AFFINITY SELECTION-BASED SCREENING OF HYDROPHOBIC PROTEINS

<130> 10845-033001

<140> US 10/029,009

<141> 2001-12-19

<150> US 60/258,970

<151> 2000-12-29

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> epitope tag sequence

<400> 1

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 2

<211> 9

<212> PRT

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<220>

<223> epitope tag sequence

<400> 2

Glu Glu Glu Glu Tyr Met Pro Met Glu
1 5

<210> 3

<211> 9

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<213> Artificial Sequence

<220>

<223> epitope tag sequence

<400> 3

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 4

<211> 12

<212> PRT
 <213> Artificial Sequence

<220>
 <223> epitope tag sequence

<400> 4
 Lys His Lys Leu Glu Gln Leu Arg Asn Ser Gly Ala
 1 5 10

<210> 5
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> epitope tag sequence

<400> 5
 Gln Pro Glu Leu Ala Pro Glu Asp Pro Glu Asp
 1 5 10

<210> 6
 <211> 39
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> epitope tag sequence

<400> 6
 Met Asn Gly Thr Glu Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Lys
 1 5 10 15
 Thr Gly Val Val Arg Ser Pro Phe Glu Ala Pro Gln Tyr Tyr Leu Ala
 20 25 30
 Glu Pro Trp Gln Phe Ser Met
 35

<210> 7
 <211> 488
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> target sequence

<400> 7
 Met Lys His Lys Leu Glu Gln Leu Arg Asn Ser Gly Ala Glu Glu Glu
 1 5 10 15
 Glu Tyr Met Pro Met Glu Met Asn Asn Ser Thr Asn Ser Ser Asn Asn
 20 25 30
 Ser Leu Ala Leu Thr Ser Pro Tyr Lys Thr Phe Glu Val Val Phe Ile
 35 40 45
 Val Leu Val Ala Gly Ser Leu Ser Leu Val Thr Ile Ile Gly Asn Ile
 50 55 60
 Leu Val Met Val Ser Ile Lys Val Asn Arg His Leu Gln Thr Val Asn
 65 70 75 80
 Asn Tyr Phe Leu Phe Ser Leu Ala Cys Ala Asp Leu Ile Ile Gly Val
 85 90 95
 Phe Ser Met Asn Leu Tyr Thr Leu Tyr Thr Val Ile Gly Tyr Trp Pro
 100 105 110

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Leu Gly Pro Val Val Cys Asp Leu Trp Leu Ala Leu Asp Tyr Val Val
      115      120      125
Ser Asn Ala Ser Val Met Asn Leu Leu Ile Ile Ser Phe Asp Arg Tyr
      130      135      140
Phe Cys Val Thr Lys Pro Leu Thr Tyr Pro Val Lys Arg Thr Thr Lys
145      150      155      160
Met Ala Gly Met Met Ile Ala Ala Ala Trp Val Leu Ser Phe Ile Leu
      165      170      175
Trp Ala Pro Ala Ile Leu Phe Trp Gln Phe Ile Val Gly Val Arg Thr
      180      185      190
Val Glu Asp Gly Glu Cys Tyr Ile Gln Phe Phe Ser Asn Ala Ala Val
      195      200      205
Thr Phe Gly Thr Ala Ile Ala Ala Phe Tyr Leu Pro Val Ile Ile Met
      210      215      220
Thr Val Leu Tyr Trp His Ile Ser Arg Ala Ser Lys Ser Arg Ile Lys
225      230      235      240
Lys Asp Lys Lys Glu Pro Val Ala Asn Gln Asp Pro Val Ser Pro Ser
      245      250      255
Leu Val Gln Gly Arg Ile Val Lys Pro Asn Asn Asn Asn Met Pro Ser
      260      265      270
Ser Asp Asp Gly Leu Glu His Asn Lys Ile Gln Asn Gly Lys Ala Pro
      275      280      285
Arg Asp Pro Val Thr Glu Asn Cys Val Gln Gly Glu Glu Lys Glu Ser
      290      295      300
Ser Asn Asp Ser Thr Ser Val Ser Ala Val Ala Ser Asn Met Arg Asp
305      310      315      320
Asp Glu Ile Thr Gln Asp Glu Asn Thr Val Ser Thr Ser Leu Gly His
      325      330      335
Ser Lys Asp Glu Asn Ser Lys Gln Thr Cys Ile Arg Ile Gly Thr Lys
      340      345      350
Thr Pro Lys Ser Asp Ser Cys Thr Pro Thr Asn Thr Thr Val Glu Val
      355      360      365
Val Gly Ser Ser Gly Gln Asn Gly Asp Glu Lys Gln Asn Ile Val Ala
      370      375      380
Arg Lys Ile Val Lys Met Thr Lys Gln Pro Ala Lys Lys Lys Pro Pro
385      390      395      400
Pro Ser Arg Glu Lys Lys Val Thr Arg Thr Ile Leu Ala Ile Leu Leu
      405      410      415
Ala Phe Ile Ile Thr Trp Ala Pro Tyr Asn Val Met Val Leu Ile Asn
      420      425      430
Thr Phe Cys Ala Pro Cys Ile Pro Asn Thr Val Trp Thr Ile Gly Tyr
      435      440      445
Trp Leu Cys Tyr Ile Asn Ser Thr Ile Asn Pro Ala Cys Tyr Ala Leu
      450      455      460
Cys Asn Ala Thr Phe Lys Lys Thr Phe Lys His Leu Leu Met Cys His
465      470      475      480
Tyr Lys Asn Ile Gly Ala Thr Arg
      485

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<210> 8

<211> 431

<212> PRT

<213> Artificial Sequence

<220>

<223> target sequence

<400> 8

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Met Asp Tyr Lys Asp Asp Asp Asp Lys Met Gly Gln Pro Gly Asn Gly
1      5      10      15
Ser Ala Phe Leu Leu Ala Pro Asn Arg Ser His Ala Pro Asp His Asp

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				20						25				30		
Val	Thr	Gln	Gln	Arg	Asp	Glu	Val	Trp	Val	Val	Gly	Met	Gly	Ile	Val	
		35					40					45				
Met	Ser	Leu	Ile	Val	Leu	Ala	Ile	Val	Phe	Gly	Asn	Val	Leu	Val	Ile	
	50					55					60					
Thr	Ala	Ile	Ala	Lys	Phe	Glu	Arg	Leu	Gln	Thr	Val	Thr	Asn	Tyr	Phe	
65					70					75					80	
Ile	Thr	Ser	Leu	Ala	Cys	Ala	Asp	Leu	Val	Met	Gly	Leu	Ala	Val	Val	
				85					90						95	
Pro	Phe	Gly	Ala	His	Ile	Leu	Met	Lys	Met	Trp	Thr	Phe	Gly	Asn		
			100				105						110			
Phe	Trp	Cys	Glu	Phe	Trp	Thr	Ser	Ile	Asp	Val	Leu	Cys	Val	Thr	Ala	
		115					120					125				
Ser	Ile	Glu	Thr	Leu	Cys	Val	Ile	Ala	Val	Asp	Arg	Tyr	Phe	Ala	Ile	
	130					135						140				
Thr	Ser	Pro	Phe	Lys	Tyr	Gln	Ser	Leu	Leu	Thr	Lys	Asn	Lys	Ala	Arg	
145					150					155					160	
Val	Ile	Ile	Leu	Met	Val	Trp	Ile	Val	Ser	Gly	Leu	Thr	Ser	Phe	Leu	
				165					170						175	
Pro	Ile	Gln	Met	His	Trp	Tyr	Arg	Ala	Thr	His	Gln	Glu	Ala	Ile	Asn	
			180					185					190			
Cys	Tyr	Ala	Asn	Glu	Thr	Cys	Cys	Asp	Phe	Phe	Thr	Asn	Gln	Ala	Tyr	
		195					200					205				
Ala	Ile	Ala	Ser	Ser	Ile	Val	Ser	Phe	Tyr	Val	Pro	Leu	Val	Ile	Met	
	210					215					220					
Val	Phe	Val	Tyr	Ser	Arg	Val	Phe	Gln	Glu	Ala	Lys	Arg	Gln	Leu	Gln	
225					230					235					240	
Lys	Ile	Asp	Lys	Ser	Glu	Gly	Arg	Phe	His	Val	Gln	Asn	Leu	Ser	Gln	
				245					250						255	
Val	Glu	Gln	Asp	Gly	Arg	Thr	Gly	His	Gly	Leu	Arg	Arg	Ser	Ser	Lys	
			260					265					270			
Phe	Cys	Leu	Lys	Glu	His	Lys	Ala	Leu	Lys	Thr	Leu	Gly	Ile	Ile	Met	
		275					280					285				
Gly	Thr	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Phe	Ile	Val	Asn	Ile	Val	
	290					295					300					
His	Val	Ile	Gln	Asp	Asn	Leu	Ile	Arg	Lys	Glu	Val	Tyr	Ile	Leu	Leu	
305					310					315					320	
Asn	Trp	Ile	Gly	Tyr	Val	Asn	Ser	Gly	Phe	Asn	Pro	Leu	Ile	Tyr	Cys	
				325					330						335	
Arg	Ser	Pro	Asp	Phe	Arg	Ile	Ala	Phe	Gln	Glu	Leu	Leu	Cys	Leu	Arg	
			340					345					350			
Arg	Ser	Ser	Leu	Lys	Ala	Tyr	Gly	Asn	Gly	Tyr	Ser	Ser	Asn	Gly	Asn	
		355					360					36				

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<210> 9
<211> 488
<212> PRT
<213> Artificial Sequence
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<220>
<223> target sequence

<400> 9

Met	Ala	Thr	Leu	Pro	Ala	Ala	Glu	Thr	Trp	Ile	Asp	Gly	Gly	Gly	Gly	1	5	10	15
Val	Gly	Ala	Asp	Ala	Val	Asn	Leu	Thr	Ala	Ser	Leu	Ala	Ala	Gly	Ala	20	25	30	
Ala	Thr	Gly	Ala	Val	Glu	Thr	Gly	Trp	Leu	Gln	Leu	Leu	Asp	Gln	Ala	35	40	45	
Gly	Asn	Leu	Ser	Ser	Ser	Pro	Ser	Ala	Leu	Gly	Leu	Pro	Val	Ala	Ser	50	55	60	
Pro	Ala	Pro	Ser	Gln	Pro	Trp	Ala	Asn	Leu	Thr	Asn	Gln	Phe	Val	Gln	65	70	75	80
Pro	Ser	Trp	Arg	Ile	Ala	Leu	Trp	Ser	Leu	Ala	Tyr	Gly	Val	Val	Val	85	90	95	
Ala	Val	Ala	Val	Leu	Gly	Asn	Leu	Ile	Val	Ile	Trp	Ile	Ile	Leu	Ala	100	105	110	
His	Lys	Arg	Met	Arg	Thr	Val	Thr	Asn	Tyr	Phe	Leu	Val	Asn	Leu	Ala	115	120	125	
Phe	Ser	Asp	Ala	Ser	Met	Ala	Ala	Phe	Asn	Thr	Leu	Val	Asn	Phe	Ile	130	135	140	
Tyr	Ala	Leu	His	Ser	Glu	Trp	Tyr	Phe	Gly	Ala	Asn	Tyr	Cys	Arg	Phe	145	150	155	160
Gln	Asn	Phe	Phe	Pro	Ile	Thr	Ala	Val	Phe	Ala	Ser	Ile	Tyr	Ser	Met	165	170	175	
Thr	Ala	Ile	Ala	Val	Asp	Arg	Tyr	Met	Ala	Ile	Ile	Asp	Pro	Leu	Lys	180	185	190	
Pro	Arg	Leu	Ser	Ala	Thr	Ala	Thr	Lys	Ile	Val	Ile	Gly	Ser	Ile	Trp	195	200	205	
Ile	Leu	Ala	Phe	Leu	Leu	Ala	Phe	Pro	Gln	Cys	Leu	Tyr	Ser	Lys	Thr	210	215	220	
Lys	Val	Met	Pro	Gly	Arg	Thr	Leu	Cys	Phe	Val	Gln	Trp	Pro	Glu	Gly	225	230	235	240
Pro	Lys	Gln	His	Phe	Thr	Tyr	His	Ile	Ile	Val	Ile	Ile	Leu	Val	Tyr	245	250	255	
Cys	Phe	Pro	Leu	Leu	Ile	Met	Gly	Ile	Thr	Tyr	Thr	Ile	Val	Gly	Ile	260	265	270	
Thr	Leu	Trp	Gly	Gly	Glu	Ile	Pro	Gly	Asp	Thr	Cys	Asp	Lys	Tyr	His	275	280	285	
Glu	Gln	Leu	Lys	Ala	Lys	Arg	Lys	Val	Val	Lys	Met	Met	Ile	Ile	Val	290	295	300	
Val	Met	Thr	Phe	Ala	Ile	Cys	Trp	Leu	Pro	Tyr	His	Ile	Tyr	Phe	Ile	305	310	315	320
Leu	Thr	Ala	Ile	Tyr	Gln	Gln	Leu	Asn	Arg	Trp	Lys	Tyr	Ile	Gln	Gln	325	330	335	
Val	Tyr	Leu	Ala	Ser	Phe	Trp	Leu	Ala	Met	Ser	Ser	Thr	Met	Tyr	Asn	340	345	350	
Pro	Ile	Ile	Tyr	Cys	Cys	Leu	Asn	Lys	Arg	Phe	Arg	Ala	Gly	Phe	Lys	355	360	365	
Arg	Ala	Phe	Arg	Trp	Cys	Pro	Phe	Ile	Lys	Val	Ser	Ser	Tyr	Asp	Glu	370	375	380	
Leu	Glu	Leu	Lys	Thr	Thr	Arg	Phe	His	Pro	Asn	Arg	Gln	Ser	Ser	Met	385	390	395	400
Tyr	Thr	Val	Thr	Arg	Met	Glu	Ser	Met	Thr	Val	Val	Phe	Asp	Pro	Asn	405	410	415	
Asp	Ala	Asp	Thr	Thr	Arg	Ser	Ser	Arg	Lys	Lys	Arg	Ala	Thr	Pro	Arg	420	425	430	
Asp	Pro	Ser	Phe	Asn	Gly	Cys	Ser	Arg	Arg	Asn	Ser	Lys	Ser	Ala	Ser	435	440	445	
Ala	Thr	Ser	Ser	Phe	Ile	Ser	Ser	Pro	Tyr	Thr	Ser	Val	Asp	Glu	Tyr	450	455	460	
Ser	Gln	Pro	Glu	Leu	Ala	Pro	Glu	Asp	Pro	Glu	Asp	Lys	His	Lys	Leu	465	470	475	480
Glu	Gln	Leu	Arg	Asn	Ser	Gly	Ala												

485

<210> 10
 <211> 478
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> target sequence

<400> 10
 Met Asp Tyr Lys Asp Asp Asp Asp Lys Met Asn Thr Ser Ala Pro Pro
 1 5 10 15
 Ala Val Ser Pro Asn Ile Thr Val Leu Ala Pro Gly Lys Gly Pro Trp
 20 25 30
 Gln Val Ala Phe Ile Gly Ile Thr Thr Gly Leu Leu Ser Leu Ala Thr
 35 40 45
 Val Thr Gly Asn Leu Leu Val Leu Ile Ser Phe Lys Val Asn Thr Glu
 50 55 60
 Leu Lys Thr Val Asn Asn Tyr Phe Leu Leu Ser Leu Ala Cys Ala Asp
 65 70 75 80
 Leu Ile Ile Gly Thr Phe Ser Met Asn Leu Tyr Thr Thr Tyr Leu Leu
 85 90 95
 Met Gly His Trp Ala Leu Gly Thr Leu Ala Cys Asp Leu Trp Leu Ala
 100 105 110
 Leu Asp Tyr Val Ala Ser Asn Ala Ser Val Met Asn Leu Leu Leu Ile
 115 120 125
 Ser Phe Asp Arg Tyr Phe Ser Val Thr Arg Pro Leu Ser Tyr Arg Ala
 130 135 140
 Lys Arg Thr Pro Arg Arg Ala Ala Leu Met Ile Gly Leu Ala Trp Leu
 145 150 155 160
 Val Ser Phe Val Leu Trp Ala Pro Ala Ile Leu Phe Trp Gln Tyr Leu
 165 170 175
 Val Gly Glu Arg Thr Val Leu Ala Gly Gln Cys Tyr Ile Gln Phe Leu
 180 185 190
 Ser Gln Pro Ile Ile Thr Phe Gly Thr Ala Met Ala Ala Phe Tyr Leu
 195 200 205
 Pro Val Thr Val Met Cys Thr Leu Tyr Trp Arg Ile Tyr Arg Glu Thr
 210 215 220
 Glu Asn Arg Ala Arg Glu Leu Ala Ala Leu Gln Gly Ser Glu Thr Pro
 225 230 235 240
 Gly Lys Gly Gly Gly Ser Ser Ser Ser Ser Glu Arg Ser Gln Pro Gly
 245 250 255
 Ala Glu Gly Ser Pro Glu Thr Pro Pro Gly Arg Cys Cys Arg Cys Cys
 260 265 270
 Arg Ala Pro Arg Leu Leu Gln Ala Tyr Ser Trp Lys Glu Glu Glu Glu
 275 280 285
 Glu Asp Glu Gly Ser Met Glu Ser Leu Thr Ser Ser Glu Gly Glu Glu
 290 295 300
 Pro Gly Ser Glu Val Val Ile Lys Met Pro Met Val Asp Pro Glu Ala
 305 310 315 320
 Gln Ala Pro Thr Lys Gln Pro Pro Arg Ser Ser Pro Asn Thr Val Lys
 325 330 335
 Arg Pro Thr Lys Lys Gly Arg Asp Arg Ala Gly Lys Gly Gln Lys Pro
 340 345 350
 Arg Gly Lys Glu Gln Leu Ala Lys Arg Lys Thr Phe Ser Leu Val Lys
 355 360 365
 Glu Lys Lys Ala Ala Arg Thr Leu Ser Ala Ile Leu Leu Ala Phe Ile
 370 375 380
 Leu Thr Trp Thr Pro Tyr Asn Ile Met Val Leu Val Ser Thr Phe Cys
 385 390 395 400

Lys Asp Cys Val Pro Glu Thr Leu Trp Glu Leu Gly Tyr Trp Leu Cys
 405 410 415
 Tyr Val Asn Ser Thr Ile Asn Pro Met Cys Tyr Ala Leu Cys Asn Lys
 420 425 430
 Ala Phe Arg Asp Thr Phe Arg Leu Leu Leu Cys Arg Trp Asp Lys
 435 440 445
 Arg Arg Trp Arg Lys Ile Pro Lys Arg Pro Gly Ser Val His Arg Thr
 450 455 460
 Pro Ser Arg Gln Cys Glu Glu Glu Glu Tyr Met Pro Met Glu
 465 470 475

<210> 11

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> target sequence

<400> 11

Met Thr Leu His Ser Asn Ser Thr Thr Ser Pro Leu Phe Pro Asn Ile
 1 5 10 15
 Ser Ser Ser Trp Val His Ser Pro Ser Glu Ala Gly Leu Pro Leu Gly
 20 25 30
 Thr Val Thr Gln Leu Gly Ser Tyr Asn Ile Ser Gln Glu Thr Gly Asn
 35 40 45
 Phe Ser Ser Asn Asp Thr Ser Ser Asp Pro Leu Gly Gly His Thr Ile
 50 55 60
 Trp Gln Val Val Phe Ile Ala Phe Leu Thr Gly Phe Leu Ala Leu Val
 65 70 75 80
 Thr Ile Ile Gly Asn Ile Leu Val Ile Val Ala Phe Lys Val Asn Lys
 85 90 95
 Gln Leu Lys Thr Val Asn Asn Tyr Phe Leu Leu Ser Leu Ala Cys Ala
 100 105 110
 Asp Leu Ile Ile Gly Val Ile Ser Met Asn Leu Phe Thr Thr Tyr Ile
 115 120 125
 Ile Met Asn Arg Trp Ala Leu Gly Asn Leu Ala Cys Asp Leu Trp Leu
 130 135 140
 Ser Ile Asp Tyr Val Ala Ser Asn Ala Ser Val Met Asn Leu Leu Val
 145 150 155 160
 Ile Ser Phe Asp Arg Tyr Phe Ser Ile Thr Arg Pro Leu Thr Tyr Arg
 165 170 175
 Ala Lys Arg Thr Thr Lys Arg Ala Gly Val Met Ile Gly Leu Ala Trp
 180 185 190
 Val Ile Ser Phe Val Leu Trp Ala Pro Ala Ile Leu Phe Trp Gln Tyr
 195 200 205
 Phe Val Gly Lys Arg Thr Val Pro Pro Gly Glu Cys Phe Ile Gln Phe
 210 215 220
 Leu Ser Glu Pro Thr Ile Thr Phe Gly Thr Ala Ile Ala Ala Phe Tyr
 225 230 235 240
 Met Pro Val Thr Ile Met Thr Ile Leu Tyr Trp Arg Ile Tyr Lys Glu
 245 250 255
 Thr Glu Lys Arg Thr Lys Glu Leu Ala Gly Leu Gln Ala Ser Gly Thr
 260 265 270
 Glu Ala Glu Ala Glu Asn Phe Val His Pro Thr Gly Ser Ser Arg Ser
 275 280 285
 Cys Ser Ser Tyr Glu Leu Gln Gln Gly Val Lys Arg Ser Ser Arg
 290 295 300
 Arg Lys Tyr Gly Arg Cys His Phe Trp Phe Thr Thr Lys Ser Trp Lys
 305 310 315 320
 Pro Ser Ala Glu Gln Met Asp Gln Asp His Ser Ser Ser Asp Ser Trp

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          325          330          335
Asn Asn Asn Asp Ala Ala Ala Ser Leu Glu Asn Ser Ala Ser Ser Asp
          340          345          350
Glu Glu Asp Ile Gly Ser Glu Thr Arg Ala Ile Tyr Ser Ile Val Leu
          355          360          365
Lys Leu Pro Gly His Ser Ser Ile Leu Asn Ser Thr Lys Leu Pro Ser
          370          375          380
Ser Asp Asn Leu Gln Val Ser Asn Glu Asp Leu Gly Thr Val Asp Val
385          390          395          400
Glu Arg Asn Ala His Lys Leu Gln Ala Gln Lys Ser Met Gly Asp Gly
          405          410          415
Asp Asn Cys Gln Lys Asp Phe Thr Lys Leu Pro Ile Gln Leu Glu Ser
          420          425          430
Ala Val Asp Thr Gly Lys Thr Ser Asp Thr Asn Ser Ser Ala Asp Lys
          435          440          445
Thr Thr Ala Thr Leu Pro Leu Ser Phe Lys Glu Ala Thr Leu Ala Lys
          450          455          460
Arg Phe Ala Leu Lys Thr Arg Ser Gln Ile Thr Lys Arg Lys Arg Met
465          470          475          480
Ser Leu Ile Lys Glu Lys Lys Ala Ala Gln Thr Leu Ser Ala Ile Leu
          485          490          495
Leu Ala Phe Ile Ile Thr Trp Thr Pro Tyr Asn Ile Met Val Leu Val
          500          505          510
Asn Thr Phe Cys Asp Ser Cys Ile Pro Lys Thr Tyr Trp Asn Leu Gly
          515          520          525
Tyr Trp Leu Cys Tyr Ile Asn Ser Thr Val Asn Pro Val Cys Tyr Ala
          530          535          540
Leu Cys Asn Lys Thr Phe Arg Thr Thr Phe Lys Thr Leu Leu Leu Cys
545          550          555          560
Gln Cys Asp Lys Arg Lys Arg Arg Lys Gln Gln Tyr Gln Gln Arg Gln
          565          570          575
Ser Val Ile Phe His Lys Arg Val Pro Glu Gln Ala Leu Gln Pro Glu
          580          585          590
Leu Ala Pro Glu Asp Pro Glu Asp His His His His His His His His
          595          600          605

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<210> 12
 <211> 20
 <212> PRT
 <213> *Apis mellifera ligustica*

<400> 12
 Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile Ser
 1 5 10 15
 Tyr Ile Tyr Ala
 20

<210> 13
 <211> 16
 <212> PRT
 <213> *Baculovirus* sp.

<400> 13
 Val Arg Thr Ala Val Leu Ile Leu Leu Leu Val Arg Phe Ser Glu Pro
 1 5 10 15

<210> 14
 <211> 15
 <212> PRT
 <213> *Influenza A virus*

<400> 14

Lys Thr Ile Ile Ala Leu Ser Tyr Ile Phe Cys Leu Val Phe Ala
 1 5 10 15

<210> 15

<211> 34

<212> PRT

<213> Homo sapiens

<400> 15

Met Asn Gly Thr Glu Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Lys
 1 5 10 15
 Thr Gly Val Val Arg Ser Pro Phe Glu Ala Pro Gln Tyr Tyr Leu Ala
 20 25 30
 Glu Pro

<210> 16

<211> 18

<212> PRT

<213> Homo sapiens

<400> 16

Gly Lys Asn Pro Leu Gly Val Arg Lys Thr Glu Thr Ser Gln Val Ala
 1 5 10 15
 Pro Ala

<210> 17

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 17

His His His His His
 1 5

<210> 18

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 18

His His His His His His His His His His
 1 5 10

<210> 19

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> target sequence

<400> 19

Met	Val	Arg	Thr	Ala	Val	Leu	Ile	Leu	Leu	Leu	Val	Arg	Phe	Ser	Glu
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Pro	Lys	His	Lys	Leu	Glu	Gln	Leu	Arg	Asn	Ser	Gly	Ala	Ala	Ala	Glu
			20					25					30		
Glu	Glu	Glu	Tyr	Met	Pro	Met	Glu	Met	Asn	Asn	Ser	Thr	Asn	Ser	Ser
			35				40					45			
Asn	Asn	Ser	Leu	Ala	Leu	Thr	Ser	Pro	Tyr	Lys	Thr	Phe	Glu	Val	Val
			50			55					60				
Phe	Ile	Val	Leu	Val	Ala	Gly	Ser	Leu	Ser	Leu	Val	Thr	Ile	Ile	Gly
65					70					75					80
Asn	Ile	Leu	Val	Met	Val	Ser	Ile	Lys	Val	Asn	Arg	His	Leu	Gln	Thr
				85					90					95	
Val	Asn	Asn	Tyr	Phe	Leu	Phe	Ser	Leu	Ala	Cys	Ala	Asp	Leu	Ile	Ile
			100					105					110		
Gly	Val	Phe	Ser	Met	Asn	Leu	Tyr	Thr	Leu	Tyr	Thr	Val	Ile	Gly	Tyr
			115				120					125			
Trp	Pro	Leu	Gly	Pro	Val	Val	Cys	Asp	Leu	Trp	Leu	Ala	Leu	Asp	Tyr
			130			135					140				
Val	Val	Ser	Asn	Ala	Ser	Val	Met	Asn	Leu	Leu	Ile	Ile	Ser	Phe	Asp
145					150					155					160
Arg	Tyr	Phe	Cys	Val	Thr	Lys	Pro	Leu	Thr	Tyr	Pro	Val	Lys	Arg	Thr
				165					170					175	
Thr	Lys	Met	Ala	Gly	Met	Met	Ile	Ala	Ala	Ala	Trp	Val	Leu	Ser	Phe
			180					185					190		
Ile	Leu	Trp	Ala	Pro	Ala	Ile	Leu	Phe	Trp	Gln	Phe	Ile	Val	Gly	Val
			195				200					205			
Arg	Thr	Val	Glu	Asp	Gly	Glu	Cys	Tyr	Ile	Gln	Phe	Phe	Ser	Asn	Ala
			210			215					220				
Ala	Val	Thr	Phe	Gly	Thr	Ala	Ile	Ala	Ala	Phe	Tyr	Leu	Pro	Val	Ile
225					230					235					240
Ile	Met	Thr	Val	Leu	Tyr	Trp	His	Ile	Ser	Arg	Ala	Ser	Lys	Ser	Arg
				245					250					255	
Ile	Lys	Lys	Asp	Lys	Lys	Glu	Pro	Val	Ala	Asn	Gln	Asp	Pro	Val	Ser
			260					265					270		
Pro	Ser	Leu	Val	Gln	Gly	Arg	Ile	Val	Lys	Pro	Asn	Asn	Asn	Asn	Met
			275				280					285			
Pro	Ser	Ser	Asp	Asp	Gly	Leu	Glu	His	Asn	Lys	Ile	Arg	Asp	Pro	Val
			290			295					300				
Thr	Glu	Asn	Cys	Val	Gln	Gly	Glu	Glu	Lys	Glu	Ser	Ser	Asn	Asp	Ser
305					310					315					320
Thr	Ser	Val	Ser	Ala	Val	Ala	Ser	Asn	Met	Arg	Asp	Asp	Glu	Ile	Thr
				325					330					335	
Gln	Asp	Glu	Asn	Thr	Val	Ser	Thr	Ser	Leu	Gly	His	Ser	Lys	Asp	Glu
			340					345					350		
Asn	Ser	Lys	Gln	Thr	Cys	Ile	Arg	Ile	Gly	Thr	Lys	Thr	Pro	Lys	Ser
			355				360					365			
Asp	Ser	Cys	Thr	Pro	Thr	Asn	Thr	Thr	Val	Glu	Val	Val	Gly	Ser	Ser
			370			375					380				
Gly	Gln	Asn	Gly	Asp	Glu	Lys	Gln	Asn	Ile	Val	Ala	Arg	Lys	Ile	Val
385					390					395					400
Lys	Met	Thr	Lys	Gln	Pro	Ala	Lys	Lys	Lys	Pro	Pro	Pro	Ser	Arg	Glu
				405					410					415	
Lys	Lys	Val	Thr	Arg	Thr	Ile	Leu	Ala	Ile	Leu	Leu	Ala	Phe	Ile	Ile
			420					425					430		
Thr	Trp	Ala	Pro	Tyr	Asn	Val	Met	Val	Leu	Ile	Asn	Thr	Phe	Cys	Ala
			435			440						445			
Pro	Cys	Ile	Pro	Asn	Thr	Val	Trp	Thr	Ile	Gly	Tyr	Trp	Leu	Cys	Tyr
			450			455					460				
Ile	Asn	Ser	Thr	Ile	Asn	Pro	Ala	Cys	Tyr	Ala	Leu	Cys	Asn	Ala	Thr
465					470					475					480
Phe	Lys	Lys	Thr	Phe	Lys	His	Leu	Leu	Met	Cys	His	Tyr	Lys	Asn	Ile

	485							490						495			
Gly Ala Thr Arg 500																	
<210>	20																
<211>	451																
<212>	PRT																
<213>	Artificial Sequence																
<220>																	
<223>	target sequence																
<400>	20																
Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile 1 5 10 15																	
Ser Tyr Ile Tyr Ala Asp Tyr Lys Asp Asp Asp Lys Met Gly Gln 20 25 30																	
Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg Ser His Ala 35 40 45																	
Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp Val Val Gly 50 55 60																	
Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val Phe Gly Asn 65 70 75 80																	
Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu Gln Thr Val 85 90 95																	
Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu Val Met Gly 100 105 110																	
Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met Lys Met Trp 115 120 125																	
Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile Asp Val Leu 130 135 140																	
Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala Val Asp Arg 145 150 155 160																	
Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu Leu Thr Lys 165 170 175																	
Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val Ser Gly Leu 180 185 190																	
Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala Thr His Gln 195 200 205																	
Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp Phe Phe Thr 210 215 220																	
Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe Tyr Val Pro 225 230 235 240																	
Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln Glu Ala Lys 245 250 255																	
Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe His Val Gln 260 265 270																	
Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His Gly Leu Arg 275 280 285																	
Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu Lys Thr Leu 290 295 300																	
Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro Phe Phe Ile 305 310 315 320																	
Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg Lys Glu Val 325 330 335																	
Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly Phe Asn Pro 340 345 350																	
Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe Gln Glu Leu 355 360 365																	
Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn Gly Tyr Ser 370 375 380																	

Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val Glu Gln Glu
 385 390 395 400
 Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr Glu Asp Phe
 405 410 415
 Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp Ser Gln Gly
 420 425 430
 Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu Glu Glu Glu Glu Tyr Met
 435 440 445
 Pro Met Glu
 450

<210> 21
 <211> 505
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> target sequence

<400> 21
 Met Lys Thr Ile Ile Ala Leu Ser Tyr Ile Phe Cys Leu Val Phe Ala
 1 5 10 15
 Met Ala Ile Leu Pro Ala Ala Glu Thr Trp Ile Asp Gly Gly Gly Gly
 20 25 30
 Val Gly Ala Asp Ala Val Asn Leu Thr Ala Ser Leu Ala Ala Gly Ala
 35 40 45
 Ala Thr Gly Ala Val Glu Thr Gly Trp Leu Gln Leu Leu Asp Gln Ala
 50 55 60
 Gly Asn Leu Ser Ser Ser Pro Ser Ala Leu Gly Leu Pro Val Arg Ser
 65 70 75 80
 Pro Ala Pro Ser Gln Pro Trp Ala Asn Leu Thr Asn Gln Phe Val Gln
 85 90 95
 Pro Ser Trp Arg Ile Ala Leu Trp Ser Leu Ala Tyr Gly Val Val Val
 100 105 110
 Ala Val Ala Val Leu Gly Asn Leu Ile Val Ile Trp Ile Ile Leu Ala
 115 120 125
 His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala
 130 135 140
 Phe Ser Asp Ala Ser Met Ala Ala Phe Asn Thr Leu Val Asn Phe Ile
 145 150 155 160
 Tyr Ala Leu His Ser Glu Trp Tyr Phe Gly Ala Asn Tyr Cys Arg Phe
 165 170 175
 Gln Asn Phe Phe Pro Ile Thr Ala Val Phe Ala Ser Ile Tyr Ser Met
 180 185 190
 Thr Ala Ile Ala Val Asp Arg Tyr Met Ala Ile Ile Asp Pro Leu Lys
 195 200 205
 Pro Arg Leu Ser Ala Thr Ala Thr Lys Ile Val Ile Gly Ser Ile Trp
 210 215 220
 Ile Leu Ala Phe Leu Leu Ala Phe Pro Gln Cys Leu Tyr Ser Lys Thr
 225 230 235 240
 Lys Val Met Pro Gly Arg Thr Leu Cys Phe Val Gln Trp Pro Glu Gly
 245 250 255
 Pro Lys Gln His Phe Thr Tyr His Ile Ile Val Ile Ile Leu Val Tyr
 260 265 270
 Cys Phe Pro Leu Leu Ile Met Gly Ile Thr Tyr Thr Ile Val Gly Ile
 275 280 285
 Thr Leu Trp Gly Gly Glu Ile Pro Gly Asp Thr Cys Asp Lys Tyr His
 290 295 300
 Glu Gln Leu Lys Ala Lys Arg Lys Val Val Lys Met Met Ile Ile Val
 305 310 315 320
 Val Met Thr Phe Ala Ile Cys Trp Leu Pro Tyr His Ile Tyr Phe Ile

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          325          330          335
Leu Thr Ala Ile Tyr Gln Gln Leu Asn Arg Trp Lys Tyr Ile Gln Gln
          340          345          350
Val Tyr Leu Ala Ser Phe Trp Leu Ala Met Ser Ser Thr Met Tyr Asn
          355          360          365
Pro Ile Ile Tyr Cys Cys Leu Asn Lys Arg Phe Arg Ala Gly Phe Lys
          370          375          380
Arg Ala Phe Arg Trp Cys Pro Phe Ile Lys Val Ser Ser Tyr Asp Glu
          385          390          395          400
Leu Glu Leu Lys Thr Thr Arg Phe His Pro Asn Arg Gln Ser Ser Met
          405          410          415
Tyr Thr Val Thr Arg Met Glu Ser Met Thr Val Val Phe Asp Pro Asn
          420          425          430
Asp Ala Asp Thr Thr Arg Ser Ser Arg Lys Lys Arg Ala Thr Pro Arg
          435          440          445
Asp Pro Ser Phe Asn Gly Cys Ser Arg Arg Asn Ser Lys Ser Ala Ser
          450          455          460
Ala Thr Ser Ser Phe Ile Ser Ser Pro Tyr Thr Ser Val Asp Glu Tyr
          465          470          475          480
Ser Gln Pro Glu Leu Ala Pro Glu Asp Pro Glu Asp Ala Ala Lys His
          485          490          495
Lys Leu Glu Gln Leu Arg Asn Ser Gly
          500          505

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<210> 22

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> target sequence

<400> 22

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Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
 1          5          10          15
Ser Tyr Ile Tyr Ala Asp Tyr Lys Asp Asp Asp Asp Lys Met Asn Thr
          20          25          30
Ser Ala Pro Pro Ala Val Ser Pro Asn Ile Thr Val Leu Ala Pro Gly
          35          40          45
Lys Gly Pro Trp Gln Val Ala Phe Ile Gly Ile Thr Thr Gly Leu Leu
          50          55          60
Ser Leu Ala Thr Val Thr Gly Asn Leu Leu Val Leu Ile Ser Phe Lys
          65          70          75          80
Val Asn Thr Glu Leu Lys Thr Val Asn Asn Tyr Phe Leu Leu Ser Leu
          85          90          95
Ala Cys Ala Asp Leu Ile Ile Gly Thr Phe Ser Met Asn Leu Tyr Thr
          100          105          110
Thr Tyr Leu Leu Met Gly His Trp Ala Leu Gly Thr Leu Ala Cys Asp
          115          120          125
Leu Trp Leu Ala Leu Asp Tyr Val Ala Ser Asn Ala Ser Val Met Asn
          130          135          140
Leu Leu Leu Ile Ser Phe Asp Arg Tyr Phe Ser Val Thr Arg Pro Leu
          145          150          155          160
Ser Tyr Arg Ala Lys Arg Thr Pro Arg Arg Ala Ala Leu Met Ile Gly
          165          170          175
Leu Ala Trp Leu Val Ser Phe Val Leu Trp Ala Pro Ala Ile Leu Phe
          180          185          190
Trp Gln Tyr Leu Val Gly Glu Arg Thr Val Leu Ala Gly Gln Cys Tyr
          195          200          205
Ile Gln Phe Leu Ser Gln Pro Ile Ile Thr Phe Gly Thr Ala Met Ala
          210          215          220

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Ala Phe Tyr Leu Pro Val Thr Val Met Cys Thr Leu Tyr Trp Arg Ile
 225 230 235 240
 Tyr Arg Glu Thr Glu Asn Arg Ala Arg Glu Leu Ala Ala Leu Gln Gly
 245 250 255
 Ser Glu Thr Pro Gly Lys Gly Gly Gly Ser Ser Ser Ser Ser Glu Arg
 260 265 270
 Ser Gln Pro Gly Ala Glu Gly Ser Pro Glu Thr Pro Pro Gly Arg Cys
 275 280 285
 Cys Arg Cys Cys Arg Ala Pro Arg Leu Leu Gln Ala Tyr Ser Trp Lys
 290 295 300
 Glu Glu Glu Glu Glu Asp Glu Gly Ser Met Glu Ser Leu Thr Ser Ser
 305 310 315 320
 Glu Gly Glu Glu Pro Gly Ser Glu Val Val Ile Lys Met Pro Met Val
 325 330 335
 Asp Pro Glu Ala Gln Ala Pro Thr Lys Gln Pro Pro Arg Ser Ser Pro
 340 345 350
 Asn Thr Val Lys Arg Pro Thr Lys Lys Gly Arg Asp Arg Ala Gly Lys
 355 360 365
 Gly Gln Lys Pro Arg Gly Lys Glu Gln Leu Ala Lys Arg Lys Thr Phe
 370 375 380
 Ser Leu Val Lys Glu Lys Lys Ala Ala Arg Thr Leu Ser Ala Ile Leu
 385 390 395 400
 Leu Ala Phe Ile Leu Thr Trp Thr Pro Tyr Asn Ile Met Val Leu Val
 405 410 415
 Ser Thr Phe Cys Lys Asp Cys Val Pro Glu Thr Leu Trp Glu Leu Gly
 420 425 430
 Tyr Trp Leu Cys Tyr Val Asn Ser Thr Ile Asn Pro Met Cys Tyr Ala
 435 440 445
 Leu Cys Asn Lys Ala Phe Arg Asp Thr Phe Arg Leu Leu Leu Leu Cys
 450 455 460
 Arg Trp Asp Lys Arg Arg Trp Arg Lys Ile Pro Lys Arg Pro Gly Ser
 465 470 475 480
 Val His Arg Thr Pro Ser Arg Gln Cys Glu Glu Glu Glu Tyr Met Pro
 485 490 495
 Met Glu

<210> 23
 <211> 626
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> target sequence

<400> 23
 Met Lys Thr Ile Ile Ala Leu Ser Tyr Ile Phe Cys Leu Val Phe Ala
 1 5 10 15
 Met Thr Leu His Ser Asn Ser Thr Thr Ser Pro Leu Phe Pro Asn Ile
 20 25 30
 Ser Ser Ser Trp Val His Ser Pro Ser Glu Ala Gly Leu Pro Leu Gly
 35 40 45
 Thr Val Thr Gln Leu Gly Ser Tyr Asn Ile Ser Gln Glu Thr Gly Asn
 50 55 60
 Phe Ser Ser Asn Asp Thr Ser Ser Asp Pro Leu Gly Gly His Thr Ile
 65 70 75 80
 Trp Gln Val Val Phe Ile Ala Phe Leu Thr Gly Phe Leu Ala Leu Val
 85 90 95
 Thr Ile Ile Gly Asn Ile Leu Val Ile Val Ala Phe Lys Val Asn Lys
 100 105 110
 Gln Leu Lys Thr Val Asn Asn Tyr Phe Leu Leu Ser Leu Ala Cys Ala

Leu Ala Pro Glu Asp Pro Glu Asp Ala Ala His His His His His
 610 615 620
 His His
 625

<210> 24
 <211> 21
 <212> PRT
 <213> *Apis mellifera ligustica*

<400> 24
 Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
 1 5 10 15
 Ser Tyr Ile Tyr Ala
 20

<210> 25
 <211> 17
 <212> PRT
 <213> *Baculovirus sp.*

<400> 25
 Met Val Arg Thr Ala Val Leu Ile Leu Leu Leu Val Arg Phe Ser Glu
 1 5 10 15
 Pro

<210> 26
 <211> 16
 <212> PRT
 <213> *Influenza A virus*

<400> 26
 Met Lys Thr Ile Ile Ala Leu Ser Tyr Ile Phe Cys Leu Val Phe Ala
 1 5 10 15

<210> 27
 <211> 35
 <212> PRT
 <213> *Homo sapiens*

<400> 27
 Met Met Asn Gly Thr Glu Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn
 1 5 10 15
 Lys Thr Gly Val Val Arg Ser Pro Phe Glu Ala Pro Gln Tyr Tyr Leu
 20 25 30
 Ala Glu Pro
 35

<210> 28
 <211> 19
 <212> PRT
 <213> *Homo sapiens*

<400> 28
 Met Gly Lys Asn Pro Leu Gly Val Arg Lys Thr Glu Thr Ser Gln Val
 1 5 10 15
 Ala Pro Ala

<210> 29
 <211> 496
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic construct

<400> 29

Met	Lys	Phe	Leu	Val	Asn	Val	Ala	Leu	Val	Phe	Met	Val	Val	Tyr	Ile	1	5	10	15
Ser	Tyr	Ile	Tyr	Ala	Asp	Tyr	Lys	Asp	Asp	Asp	Lys	Met	Met	Asn		20	25	30	
Asn	Ser	Thr	Asn	Ser	Ser	Asn	Ser	Gly	Leu	Ala	Leu	Thr	Ser	Pro	Tyr	35	40	45	
Lys	Thr	Phe	Glu	Val	Val	Phe	Ile	Val	Leu	Val	Ala	Gly	Ser	Leu	Ser	50	55	60	
Leu	Val	Thr	Ile	Ile	Gly	Asn	Ile	Leu	Val	Met	Val	Ser	Ile	Lys	Val	65	70	75	80
Asn	Arg	His	Leu	Gln	Thr	Val	Asn	Asn	Tyr	Phe	Leu	Phe	Ser	Leu	Ala	85	90	95	
Cys	Ala	Asp	Leu	Ile	Ile	Gly	Val	Phe	Ser	Met	Asn	Leu	Tyr	Thr	Leu	100	105	110	
Tyr	Thr	Val	Ile	Gly	Tyr	Trp	Pro	Leu	Gly	Pro	Val	Val	Cys	Asp	Leu	115	120	125	
Trp	Leu	Ala	Leu	Asp	Tyr	Val	Val	Ser	Asn	Ala	Ser	Val	Met	Asn	Leu	130	135	140	
Leu	Ile	Ile	Ser	Phe	Asp	Arg	Tyr	Phe	Cys	Val	Thr	Lys	Pro	Leu	Thr	145	150	155	160
Tyr	Pro	Val	Lys	Arg	Thr	Thr	Lys	Met	Ala	Gly	Met	Met	Ile	Ala	Ala	165	170	175	
Ala	Trp	Val	Leu	Ser	Phe	Ile	Leu	Trp	Ala	Pro	Ala	Ile	Leu	Phe	Trp	180	185	190	
Gln	Phe	Ile	Val	Gly	Val	Arg	Thr	Val	Glu	Asp	Gly	Glu	Cys	Tyr	Ile	195	200	205	
Gln	Phe	Phe	Ser	Asn	Ala	Ala	Val	Thr	Phe	Gly	Thr	Ala	Ile	Ala	Ala	210	215	220	
Phe	Tyr	Leu	Pro	Val	Ile	Ile	Met	Thr	Val	Leu	Tyr	Trp	His	Ile	Ser	225	230	235	240
Arg	Ala	Ser	Lys	Ser	Arg	Ile	Lys	Lys	Asp	Lys	Lys	Glu	Pro	Val	Ala	245	250	255	
Asn	Gln	Glu	Pro	Val	Ser	Pro	Ser	Leu	Val	Gln	Gly	Arg	Ile	Val	Lys	260	265	270	
Pro	Asn	Asn	Asn	Asn	Met	Pro	Gly	Ser	Asp	Glu	Ala	Leu	Glu	His	Asn	275	280	285	
Lys	Ile	Gln	Asn	Gly	Lys	Ala	Pro	Arg	Asp	Ala	Val	Thr	Glu	Asn	Cys	290	295	300	
Val	Gln	Gly	Glu	Glu	Lys	Glu	Ser	Ser	Asn	Asp	Ser	Thr	Ser	Val	Ser	305	310	315	320
Ala	Val	Ala	Ser	Asn	Met	Arg	Asp	Asp	Glu	Ile	Thr	Gln	Asp	Glu	Asn	325	330	335	
Thr	Val	Ser	Thr	Ser	Leu	Gly	His	Ser	Lys	Asp	Glu	Asn	Ser	Lys	Gln	340	345	350	
Thr	Cys	Ile	Lys	Ile	Val	Thr	Lys	Thr	Gln	Lys	Ser	Asp	Ser	Cys	Thr	355	360	365	
Pro	Ala	Asn	Thr	Thr	Val	Glu	Leu	Val	Gly	Ser	Ser	Gly	Gln	Asn	Gly	370	375	380	
Asp	Glu	Lys	Gln	Asn	Ile	Val	Ala	Arg	Lys	Ile	Val	Lys	Met	Thr	Lys	385	390	395	400
Gln	Pro	Ala	Lys	Lys	Lys	Pro	Pro	Pro	Ser	Arg	Glu	Lys	Lys	Val	Thr	405	410	415	

Arg	Thr	Ile	Leu	Ala	Ile	Leu	Leu	Ala	Phe	Ile	Ile	Thr	Trp	Ala	Pro
			420					425					430		
Tyr	Asn	Val	Met	Val	Leu	Ile	Asn	Thr	Phe	Cys	Ala	Pro	Cys	Ile	Pro
		435					440					445			
Asn	Thr	Val	Trp	Thr	Ile	Gly	Tyr	Trp	Leu	Cys	Tyr	Ile	Asn	Ser	Thr
	450					455					460				
Ile	Asn	Pro	Ala	Cys	Tyr	Ala	Leu	Cys	Asn	Ala	Thr	Phe	Lys	Lys	Thr
465					470					475					480
Phe	Lys	His	Leu	Leu	Met	Cys	His	Tyr	Lys	Asn	Ile	Gly	Ala	Thr	Arg
			485						490					495	